



4-31452A.ST25.txt
SEQUENCE LISTING

<110> Novartis AG
<120> Adenovirus particles with mutagenized fiber proteins
<130> 4-31452A
<140> US 09/870,203
<141> 2001-05-30
<160> 43
<170> PatentIn version 3.1
<210> 1
<211> 1746
<212> DNA
<213> Human adenovirus type 5
<220>
<221> CDS
<222> (1)..(1746)
<223>

<400> 1
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44 1
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

4-31452A.ST25.txt

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	1		
92			
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu			
50	55	60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	2		
40			
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser			
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	2		
88			
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			
85	90	95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	3		
36			
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
100	105	110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	3		
84			
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	4		
32			
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
130	135	140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	4		
80			
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln			
145	150	155	160

4-31452A.ST25.txt

aca tca ggc ccc ctc acc acc acc acc gat agc agt acc ctt act atc act 5
28 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

4-31452A.ST25.txt

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 ^ 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

4-31452A.ST25.txt

370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12 00 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12 48 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12 96 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13 44 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
435	440	445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13 92 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
450	455	460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14 40 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
465	470	475	480
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14 88 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			

4-31452A.ST25.txt

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa 17
46

Tyr Ile Ala Gln Glu

580

4-31452A.ST25.txt

<211> 581

<212> PRT

<213> Human adenovirus type 5

<400> 2

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

4-31452A.ST25.txt

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

4-31452A.ST25.txt

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

```
<210> 3
<211> 1746
<212> DNA
<213> Artificial Sequence
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<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)
<223>

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<220>
<221> mutation
<222> (1222)..(1227)
<223>
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<400> 3
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

4-31452A.ST25.txt

35	40	45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu			1
50	55	60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser			2
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			2
85	90		95
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			3
100	105		110
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			3
115	120		125
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			4
130	135		140
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 80			4

4-31452A.ST25.txt

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210 215 220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt

8

4-31452A.ST25.txt

16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
60

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

4-31452A.ST25.txt

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12
 48 Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
 405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
 96 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
 44 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
 92 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
 40 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480

4-31452A.ST25.txt

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

tac att gcc caa gaa taa 17
46 Tyr Ile Ala Gln Glu
580

4-31452A.ST25.txt

<210> 4
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<400> 4

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

4-31452A.ST25.txt

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

4-31452A.ST25.txt

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 5

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted.

<220>

<221> CDS

<222> (1)..(1740)

<223>

<400> 5

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

4-31452A.ST25.txt

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

4-31452A.ST25.txt

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
 80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
 28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
 76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
 24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
 72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
 20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
 68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

4-31452A.ST25.txt

245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04			

4-31452A.ST25.txt

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13
44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13
92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14

4-31452A.ST25.txt

40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg 14
88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt 15
36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15
84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16
32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa
 40
 Ala Gln Glu

<210> 6
 <211> 579
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted.

<400> 6

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro
1														15	

Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro
														30	
20								25							

Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
35						40						45			

Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
50						55						60			

Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70				75			80			

Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn
85									90			95			

Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu
100								105					110		

4-31452A.ST25.txt

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

4-31452A.ST25.txt

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
485 490 495

4-31452A.ST25.txt

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 7

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Combination of the mutant fiber encoded in Seq ID: #3 & 5.

<220>

<221> CDS

<222> (1)..(1740)

<223>

<400> 7

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

4-31452A.ST25.txt

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

4-31452A.ST25.txt

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att
32

4

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa
80

4

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act
28

5

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg
76

5

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg
24

6

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
72

6

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
20

7

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

4-31452A.ST25.txt

225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56			

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13
44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13

4-31452A.ST25.txt

92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

ctc ctc aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14
40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg 14
88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt 15
36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15
84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16
32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

4-31452A.ST25.txt

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

gcc caa gaa taa 17
40
Ala Gln Glu

<210> 8
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb in ation of the mutant fiber encoded in Seq ID: #3 & 5.

<400> 8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

4-31452A.ST25.txt

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

4-31452A.ST25.txt

275

280

285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

4-31452A.ST25.txt

465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
485 490 495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 9
<211> 1743
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acid 441(V) of wild-type fiber was deleted.

<220>
<221> CDS
<222> (1)..(1743)
<223>

4-31452A.ST25.txt

<400> 9
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

4-31452A.ST25.txt

100

105

110

act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
 84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
 32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
 80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
 28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
 76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
 24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
 72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

4-31452A.ST25.txt

210	215	220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20			7
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			
225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68			7
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16			8
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64			8
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12			9
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60			9
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08			10

4-31452A.ST25.txt

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct 13

4-31452A.ST25.txt

44

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser

435

440

445

gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga

13

92

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly

450

455

460

gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga

14

40

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg

465

470

475

480

aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt

14

88

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe

485

490

495

atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa

15

36

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys

500

505

510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct

15

84

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca

16

32

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

4-31452A.ST25.txt

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545 550 555 560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565 570 575

att gcc caa gaa taa 17
43

Ile Ala Gln Glu

580

<210> 10

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acid 441(V) of wild-type fiber was deleted.

<400> 10

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

4-31452A.ST25.txt

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

4-31452A.ST25.txt

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

4-31452A.ST25.txt

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
530 535 540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
565 570 575

Ile Ala Gln Glu
580

<210> 11
<211> 1743
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le

4-31452A.ST25.txt

s
otides corresponding to amino acid 442(K) of wild-type fiber wa
deleted.

<220>

<221> CDS

<222> (1)..(1743)

<223>

<400> 11

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

2

4-31452A.ST25.txt

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6

4-31452A.ST25.txt

24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac
12

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

4-31452A.ST25.txt

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Leu Glu
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
 48
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415

4-31452A.ST25.txt

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

ctt gct aca gtt tca gtt ttg gct gtt ggc agt ttg gct cca ata tct 13
44 Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
435 440 445

gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga 13
92 Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga 14
40 Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt 14
88 Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa 15
36 Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15
84 Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

4-31452A.ST25.txt

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16
32

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530 535 540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545 550 555 560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565 570 575

att gcc caa gaa taa 17
43

Ile Ala Gln Glu

580

<210> 12

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acid 442(K) of wild-type fiber was deleted.

<400> 12

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

4-31452A.ST25.txt

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

4-31452A.ST25.txt

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

4-31452A.ST25.txt

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
530 535 540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
565 570 575

Ile Ala Gln Glu
580

4-31452A.ST25.txt

<210> 13
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)
<223>

<220>
<221> mutation
<222> (1321)..(1326)
<223>

<400> 13
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

4-31452A.ST25.txt

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg
 76

5

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg
 24

6

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
 72

6

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
 20

7

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca
 68

7

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt
 16

8

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag
 64

8

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

4-31452A.ST25.txt

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
60

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12.
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gct gct gca ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Ala Gly Ser Leu Ala Pro Ile

435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc

15

4-31452A.ST25.txt

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa

15

84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac

16

32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc

16

80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca

17

28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

17

46

Tyr Ile Ala Gln Glu

580

<210> 14

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

4-31452A.ST25.txt

<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<400> 14

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

4-31452A.ST25.txt

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

4-31452A.ST25.txt

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580 ,

<210> 15
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)
<223>

<220>
<221> mutation
<222> (1378)..(1380)
<223>

<400> 15
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44 1
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

4-31452A.ST25.txt

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

4-31452A.ST25.txt

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act
28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210 215 220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

4-31452A.ST25.txt

260 265 270
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370	375	380
-----	-----	-----

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385	390	395	400
-----	-----	-----	-----

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405	410	415
-----	-----	-----

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420	425	430
-----	-----	-----

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435	440	445
-----	-----	-----

tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn

450	455	460
-----	-----	-----

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465	470	475	480
-----	-----	-----	-----

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14

4-31452A.ST25.txt

88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa 17

46

Tyr Ile Ala Gln Glu

580

4-31452A.ST25.txt

<210> 16
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.
<400> 16

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

4-31452A.ST25.txt

145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

4-31452A.ST25.txt

340

345

350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

4-31452A.ST25.txt

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 17

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted.

<220>

<221> CDS

<222> (1)..(1740)

<223>

<400> 17

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

4-31452A.ST25.txt

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 44 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	1		
35	40	45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	1		
50	55	60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	2		
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	2		
85	90	95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	3		
100	105	110	
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	3		
115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	4		
130	135	140	

4-31452A.ST25.txt

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210 215 220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245 250 255

4-31452A.ST25.txt

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

4-31452A.ST25.txt

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
 48 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
 96 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
 44 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
 92 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
 40 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

4-31452A.ST25.txt

465	470	475	480	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 88				14
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				
485	490	495		
ttt atg cct aac cta tca gct tat cca aaa tct cac act gcc aaa agt 36				15
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser				
500	505	510		
aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 84				15
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val				
515	520	525		
aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 32				16
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr				
530	535	540		
cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 80				16
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn				
545	550	555	560	
tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 28				17
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile				
565	570	575		
gcc caa gaa taa 40				17

4-31452A.ST25.txt

Ala Gln Glu

<210> 18
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted.

<400> 18

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

4-31452A.ST25.txt

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

4-31452A.ST25.txt

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

4-31452A.ST25.txt

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 19
<211> 1740
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 538(G) & 539(T) of wild-type fiber were deleted.

<220>
<221> CDS
<222> (1)..(1740)
<223>

<400> 19
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

4-31452A.ST25.txt

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

1

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

1

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

2

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

2

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

3

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

4-31452A.ST25.txt

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
 32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
 80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
 28

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
 76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
 24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
 72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
 20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

4-31452A.ST25.txt

225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56			

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13

4-31452A.ST25.txt

92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac cag gaa aca gga gac aca act 16
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

4-31452A.ST25.txt

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565 570 575

gcc caa gaa taa 17
40
Ala Gln Glu

<210> 20
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 538(G) & 539(T) of wild-type fiber were deleted.

<400> 20

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

4-31452A.ST25.txt

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

4-31452A.ST25.txt

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

4-31452A.ST25.txt

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)...(38)
<223>

<400> 21

4-31452A.ST25.txt

accacaccag ctccagaggc taactgtaga ctaaatgc
38

<210> 22
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)
<223>

<400> 22
gcatttagtc tacagttagc ctctggagct ggtgtgtt
38

<210> 23
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)
<223>

<400> 23
acagtttcag ttttggccgg cagtttggtt ccaatatac
38

<210> 24
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

4-31452A.ST25.txt

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(38)

<223>

<400> 24

gatattggag ccaaactgcc ggccaaaact gaaactgt

38

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 25

acagtttcag ttttggctaa aggcagtttg gctcca

36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 26

tggagccaaa ctgccttag ccaaaaactga aactgt

<210> 27
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 27
gtttcagttt tggctgttgg cagttggct ccaata
36

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 28
tattggagcc aaactgccaa cagccaaaac tgaaac
36

<210> 29
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

4-31452A.ST25.txt

```
<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 29
gtttcagttt tggctgctgc aggcaagttt gctcca
36

<210> 30
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 30
tggagccaaa ctgcctgcag cagccaaaac tgaaac
36

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 31
gctcatctta ttatagaatt cgacgaaaat ggagtg
36
```

4-31452A.ST25.txt

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 32
cactccattt tcgtcgaatt ctataataag atgagc
36

<210> 33
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(39)
<223>

<400> 33
gcttatccaa aatctcacac tgccaaaagt aacattgtc
39

<210> 34
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

4-31452A.ST25.txt

<220>
<221> primer_bind
<222> (1)..(39)
<223>

<400> 34
gacaatgtta cttttggcag tgtgagattt tggataaagc
39

<210> 35
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(35)
<223>

<400> 35
ctaacattt cactaaacca ggaaacagga gacac
35

<210> 36
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(35)
<223>

<400> 36
gtgtctcctg tttcctggtt tagtgtaatg gttag
35

4-31452A.ST25.txt

<210> 37
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 37
ataagatttg acgaaaactgg agtgctacta aac
33

<210> 38
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 38
gttagtgc actccagttt cgtcaaatct tat
33

<210> 39
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>

4-31452A.ST25.txt

<221> primer_bind
<222> (1)..(33)
<223>

<400> 39
tttgacgaaa atggacacct actaaacaat tcc
33

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 40
ggaattgttt agtaggtgtc cagtttcgtc aaa
33

<210> 41
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 41
aacctatcag cttatgc当地 atctcacggt aaa
33

4-31452A.ST25.txt

```
<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence
```

<220>
<223> PCR primer

```
<220>
<221> primer_bind
<222> (1)..(32)
<223>
```

<400> 42
tttaccgtga gattttgcat aagctgatag gt
32

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cRGD consensus sequence

<400> 43